

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1: MTB32A (Ra35 FL)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15	GAATACGTTG GTGTAGAAAA ATCCTGCCGC CGGGACCCCTT AAGGCTGGGA CAATTTCTGA	60
	TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTG CGCCGCGCCT CACTCAGGTG	120
	GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA	180
	GGCGGCCCG CGGGCCTTGT CGCAGGACCG GTTCGCGAC TTCCCCGCGC TGCCCCCTCGA	240
20	CCCCTCCGCG ATGGTCGCCA AAGTGGGCC ACAGGTGGTC AACATCAACA CCAAACATGGG	300
	CTACAAACAC GCGCTGGGCC CGGGGACCGG CATCGTCATC GATCCAACG GTGTCGTGCT	360
	GACAAACAAAC CACGTGATCG CGGGCGCAC CGACATCAAT CGGTTCAGCG TCGGCTCCGG	420
	CCAAACCTAC GGCGTCGATG TGGGCTGGTA TGACCGCACC CAGGATGTGC CGGTGCTGCA	480
	GCTGCGCGGT GCCGGTGGCC TGCGTCGCG GCAGCATCGGT GGCGGCGTCG CGGTGGTGA	540
25	GCCCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCGTG CGGTGCCCTGG	600
	CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GGCGCTGGAT TCGCTGACCG GTGCCGAAGA	660
	GACATTGAAC GGGTTGATCC AGTTGATGC CGCAATCCAG CCCGGTGATT CGGGCGGGCC	720
	CGTGTCAAC GGCCTAGGAC AGGTGGTCG TATGAACACG GCCGCGTCGG ATAACCTCCA	780
	GCTGTCCCAG GGTGGGCAG GATTGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGG	840
30	CCAAATCCGA TCGGGTGGGG GGTACCCAC CGTTACATAC GGGCCTACCG CCTTCCTCGG	900
	CTTGGGTGTT GTCGACAACA ACGGCAACCG CGCACGAGTC AAACGCGTGG TCGGAAGCGC	960
	TCCGGGGCA AGTCTCGGC A TCTCCACCG CGACGTGATC ACCGCGGTGG ACGGCGCTCC	1020
	GATCAACTCG GCCACCGCGA TGCGGACCG GCTTAACCGGG CATCATCCCG GTGACGTAT	1080
	CTCGGTGAAC TGGCAAACCA AGTCGGCCG CACCGTACA GGGAACGTGA CATTGGCCGA	1140
35	GGGACCCCCG GCCTGATTG TCGCGGATAC CACCCGCCGG CGGGCCAATT GGATTGGCGC	1200
	CAGCGTGAT TGCCGCGTGA GCCCCCGAGT TCCGCTCCC GTGCGCGTGG CATTGTGGAA	1260
	GCAATGAACG AGGCAGAACAA CAGCGTTGAG CACCCCTCCCG TGCAGGGCAG TTACGTCGAA	1320
	GGCGGTGTGG TCGAGCATCG GGTAGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC	1380
40	GATCCGACCT GGTAAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGC GTTCTTCGAC	1440
	GCCAGCGCGG ACGGTTCGGN CGATCTCGT GGACTCATCG ATCGCCTCGA CTACCTGCAG	1500
	TGGCTGGCA TCGACTGCAT CTGTTGGCG CGTTCCTACG ACTCACCGCT GCGCGACGGC	1560
	GGTTACGACA TTCGCGACTT CTACAAGGTG CTGCCCGAAT TCGGCACCGT CGACGATTTC	1620
	GTCGCCCTGG TCGACACCGC TCACCGCGCA GGTATCCGCA TCATCACCGA CCTGGTGATG	1680
	AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCGCGACCC AGACGGACCG	1740
	TACGGTGAAT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CGGGATCATC	1800
45	TTCGTCGACA CGAAGAGTC GAACTGGTCA TTCGATCCTG TCCGCCGACA GTTNCTACTG	1860
	GCACCGATTCTT	1872

50 (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: MTB32A (Ra35FL)

60	Met Ser Asn Ser Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser	
	1 5 10 15	
	Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala	
	20 25 30	
	Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu	
	35 40 45	
65	Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val	
	50 55 60	
	Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr	
	65 70 75 80	

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 5 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 10 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 15 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 20 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 25 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 30 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 35 Pro Pro Ala
 355

40 <212> DNA
 <213> Ra35 mature
 <400> SEQ ID NO:3

catatgcata accatcacca tcacgccccg cccgccttgt cgcaaggaccg gttcgccgac 60
 ttcccccgcg tgcggctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
 45 aacatcaaca ccaaactggg ctacaacaac gccgtggcg cccggaccgg catcgatc 180
 gatcccaacg gtgtcggtct gaccaacaac cacgtgatcg cggcgccac cgacatcaat 240
 gcgttcaagcg tcggctccgg ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc 300
 caggatgtcg cggtgctgca gctgcgcgg gccgggtggcc tgccgtcggc ggcgatcggt 360
 50 ggcggcgctcg cgggtggta gcccgtcgtc gcgatggca acagcggtgg gcaggggcgga 420
 acgccccctg cgggtccctgg cagggtggtc ggcgtcgcc aaaccgtgca ggcgtcggt 480
 tcgctgaccg gtggcgaaga gacattgaac gggttgatcc agttcgatgc cgccgatccag 540
 cccgggtgagg cggcgccggc cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg 600
 gccgcgtccg ataaacttcca gctgtccca ggtgggcagg gattcgccat tccgatcggt 660
 55 caggcgatgg cgatcgccgg ccagatccga tcgggtgggg ggtcacccac cgttcatatac 720
 gggcctaccg cttccctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
 caacgcgtgg tcgggagcgc tccggcgca agtctcggca tctccaccgg cgacgtgatc 840
 accgcgtcg acggcgctcc gatcaactcg gccaccgcga tggcgacgc gcttaacggg 900
 catcatcccg gtgacgtcat ctgcgtgacc tggcaaaccga agtcgggcgg cacgcgtaca 960
 gggAACGTGA cattggccga gggacccccc gcctgagaat tc 1002

60

<212> PRT
 <213> Ra35 mature
 <400> SEQ ID NO:4

Met His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
 5 10 15

Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
 20 25 30
 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
 5 35 40 45
 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
 50 55 60
 10 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65 70 75 80
 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
 85 90 95
 15 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 100 105 110
 20 Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val
 115 120 125
 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 130 135 140
 25 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 145 150 155 160
 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 165 170 175
 30 Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
 180 185 190
 35 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 195 200 205
 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 210 215 220
 40 Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly
 225 230 235 240
 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
 245 250 255
 45 Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 50 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 55 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330
 60
 <212> DNA
 <213> Ra35FLMutSA
 <400> SEQ ID NO:5
 65 catatgcac accatcacca tcacgccccg cggcccttgt cgaggaccg gttcgccgac 60
 ttcccccgc tgccctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
 aacatcaaca ccaaactggg ctacaacaac gccgtggcg ccgggaccgg catcgcatc 180

gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
 gcgttcagcg tcggctccgg ccaaaccctac ggcgtcgatg tggtcggta tgaccgcacc 300
 caggatgtcg cggtgctgca gctgcgcggt gccggtgcc tgccgtcgcc ggcatcggt 360
 5 ggcggcgctg cggttggta gcccgtcgtc gcatgggca acagcgggtgg gcagggcgga 420
 acgccccgtg cggtgcctgg cagggtggtc ggcgtcgcc aaaccgtgca ggcgtcggt 480
 tcgctgaccg gtgcgaaga gacattgaac gggttatcc agtgcgtatgc cgcatccag 540
 cccgggtatcg cggcgccg cgtcgtaac ggcctaggac aggtggtcgg tatgaacacg 600
 gccgcgtccg ataacttcca gctgtccca ggtggccagg gattcgccat tccgatcg 660
 10 caggcgatgg cgatcgccgg ccagatccg tcgggtgggg ggtcacccac cggtcatatc 720
 gggcctaccg ccttcctcggtt gtcgacaaca acggcaacagg cgacacgatc 780
 caacgcgtgg tcggagcgc tccggcgca agtctcgca tctccaccgg cgacgtgatc 840
 accgcggctcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
 catcatcccc gtgacgtcat ctggtgacc tggcaaaccg agtcggcgac cacgcgtaca 960
 gggAACGTGA cattggccga gggacccccc gcctgagaat tc 1002

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<212> PRT
 <213> Ra35FLMutSA
 <400> SEQ ID NO:6

20 Met His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
 5 10 15

25 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
 20 25 30

30 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
 35 40 45

35 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
 50 55 60

40 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65 70 75 80

45 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
 85 90 95

50 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 100 105 110

55 Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val
 115 120 125

60 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 130 135 140

65 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 145 150 155 160

70 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 165 170 175

75 Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
 180 185 190

80 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 195 200 205

85 Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 210 215 220

90 Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly
 225 230 235 240

95 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
 245 250 255

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
260 265 270

Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
5 275 280 285

Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
290 295 300

Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
10 305 310 315 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
325 330

15 (2) INFORMATION FOR SEQ ID NO:7: Ra35 (MTB32A N-term)

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

gccccgcggccttgcgcaggaccgttcggactttcccgccgtccccctcgaccggtcgcg
atggtcggccaagtggggccacagggtgtcaacatcaacacaaaactgggtacaacaacgcgcgtg
ggcgccgggaccggcatgtcatcgatccaaacgggtgtcgctgaccacaaccacgtgatcg
30 ggcgccacccgacatcaatgcgttcagcggtcgccggccaaacctaaccgcgtcgatgtgg
tatgaccgcacccaggatgtcgccgtgtcgacgtgcgcgggtggcctggcgtcgccgg
atcgggtggggcgtcgccgttgtgtagccgtcgatggcaacagcggtggcaggggcgga
acggccctgtgggtgcctggcagggtgtcgctcgccaaaccgtgcaggcgtcgattcqctq
35 accggtgccgaagagacattgaacgggtgatccagttcgatgccgcgatccagccgggtgaggcg
ggcgggcccgctcaacggctaggacagggtggtcggtatgaacacggccgcgtcc

(2) INFORMATION FOR SEQ ID NO:8: Ra35 (MTB32A N-term)

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
50 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
Asn Ile Asn Thr Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
55 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
60 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
65 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr

Ala Ala Ser

5

(2) INFORMATION FOR SEQ ID NO:9: Ra12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGTATGAAC	ACGGCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGGTGGGC	AGGGATTTCGC	60
CATTCCGATC	GGGCAGGCAGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCACC	120
CACCGTTCAT	ATCGGGCTTA	CCGCCTTCCT	C GGCTTGGGT	GTTGTCGACA	ACAACGGCAA	180
20 CGGGCACGCA	GTCCAACGCG	TGGTCGGAG	CGCTCCGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGGCACGTC	ATCACCGCGG	TCGACGGCG	TCCGATCAAC	TCGGCCACCG	CGATGGCGGA	300
CGCGCTAAC	GGGCATCATC	CCGGTACGCT	CATCTCGGTG	AACTGGCAAA	CCAAGTCGGG	360
25 CGGCACGCGT	ACAGGAAACG	TGACATTGGC	CGAGGGACCC	CCGGCCTGAT	TTCGTGYGG	420
ATACCACCCG	CCGGCCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:10: Ra12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr	Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gln	Gly	Phe	
1					5				10					15	
Ala	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser
40						20			25				30		
Gly	Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly
						35			40			45			
Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val		
						50			55		60				
45 Val	Gly	Ser	Ala	Pro	Ala	Ala	Ser	Leu	Gly	Ile	Ser	Thr	Gly	Asp	Val
						65			70		75		80		
Ile	Thr	Ala	Val	Asp	Gly	Ala	Pro	Ile	Asn	Ser	Ala	Thr	Ala	Met	Ala
						85			90			95			
50 Asp	Ala	Leu	Asn	Gly	His	His	Pro	Gly	Asp	Val	Ile	Ser	Val	Asn	Trp
						100			105			110			
Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr	Leu	Ala	Glu
						115			120			125			
55 Gly	Pro	Pro	Ala												
			130												

(2) INFORMATION FOR SEQ ID NO:11: TbH9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCAGGT	60
CGGGGTTGCT	CGGGCGGCCT	ACGAGACGGC	GTATGGCTG	ACGGTCCCC	CGCCGGTGAT	120

	CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC	180
	CCCGGGATC CGGGTCAACG AGGCCAATA CGCGAGATG TGGGCCAAG ACGCGCCGC	240
	GATGTTGGC TAGGCCCGG CGACGGCGAC GGCGACGGCG ACAGTGTGCTGC CGTTCGAGGA	300
5	GGCGCCGGAG ATGACCGAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCAG TCGAGGAGGC	360
	CTCCGACACC GCGCGGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCAG TGAAACAGTT	420
	GGCCCAGCCC ACGCAGGGCA CCACGCCCTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT	480
	CTCGCCGCAT CGGTGCGCGA TCAGCAACAT GGTGTCGATG GCGAACAAACC ACATGTCGAT	540
	GACCAACTCG GGTGTCGAG TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC	600
10	GGCGGGGGCC GCGCAGGGCG TGCAAACCGC GCGCAGGGGG CGATGAGCTC	660
	GCTGGGGCAGC TCGCTGGGTT CTTGGGCTCT GGGCGGTGGG GTGGCCGCA ACTTGGGTGCG	720
	GGCGGCCCTCG GTACGGTATG GTCACCGGGAA TGGCGAAAAA TATGCANAGT CTGGTCGGCG	780
	GAACGGTGGT CGCGCGTAAG GTTTACCCCCC GTTTCTGGA TGCGGTGAAC TTCGTCAACG	840
	GAAACAGTTA C	851

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: TbH9

	Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala	
	1 5 10 15	
	Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr	
	20 25 30	
30	Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu	
	35 40 45	
	Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn	
	50 55 60	
35	Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe	
	65 70 75 80	
	Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe	
	85 90 95	
	Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala	
	100 105 110	
40	Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met	
	115 120 125	
	Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly	
	130 135 140	
45	Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro	
	145 150 155 160	
	His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met	
	165 170 175	
	Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met	
	180 185 190	
50	Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala	
	195 200 205	
	Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly	
	210 215 220	
55	Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala	
	225 230 235 240	
	Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly	
	245 250 255	
	Arg Arg Asn Gly Gly Pro Ala	
	260	

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(2) INFORMATION FOR SEQ ID NO:13: TBH9FL

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5	GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
	GGCATACCCA GAGATGTTGG CGGC GGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
	TGTGGCTAGC AATGCCGCTG CGGC GGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
10	TGAGGTGTCG GCGCTGACTG CGGC GCACCT TGAGGTGTCG GCGCTGACTG CGGC GCACCT	240
	GAGCGCTCGG GCTGCTGCGA TTCA TGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
15	CTCGTATGCG GCCACTGAAG TCGCCAATGC GGCGGGGCC AGCTAAGCCA GGAACAGTCG	360
	GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGAA TTTCGGGGCG TTACCAACCGG	420
	AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCCGGCTC	480
20	AGATGTGGGA CACCGTGGCG AGTGACCTGT TTTCGGCCGC GTCCGGCTTT CAGTCGGTGG	540
	TCTGGGGTCT GACGGTGGGG TCGTGGATAG GTTCGTGCGC GGGTCTGATG GTGGCGGCCGG	600
25	CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CGCGGGGCCA GGCGAGCTG ACCGCCGCC	660
	AGGTCCGGGT TGCTGCGGCC GCCTACGAGA CGCGTATGG GCTGACGGTG CCCCCGCCGG	720
	TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
30	ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG	840
	CCCGCGATGTT TGGCTACGCC CGGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTCG	900
	AGGAGGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG	960
35	AGGCCTCCGA CACCGCCGCG GCGAACCAAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
	AGCTGGCCCA GCCCACCGAG GGCACCCACGC CTTCTTCAA GCTGGTGGC CTGTGGAAGA	1080
40	CGGTCTCGCC GCATCGGTG CCGATCAGCA ACATGGTGTG GATGGCAAC AACACATGT	1140
	CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG	1200
	CTCCGGCGGC GGCCGCCAG CGCGTGCAGA CGCGGCCAGA AAACGGGTC CGGGCGATGA	1260
45	GCTCGCTGGG CAGCTCGCTG GGTTCTTCGG GTCTGGCGG TGGGGTGGCC GCCAACTTGG	1320
	GTCGGCGGC CTCGGTCGGT TCGTTGTCGG TGCCGCAGGC CTGGGCCGCC GCCAACCAAGG	1380
50	CAGTCACCCC GGCGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG	1440
	GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG	1500
	GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG	1560
55	CCGGCTAGGA GAGGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCCG GTCTCGGTGT	1620
	TTCCCGGGCC GGCTATGACA ACAGTCAATG TGCA TGACAGGTA TTAGGTCCAG	1680
60	GTTCAACAAG GAGACAGGCA ACATGGCCTC ACAGTTTATG ACGGATCCGC ACGCGATGCG	1740
	GGACATGGCG GGCGTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT	1800
	GTGGGCCTCC GCGAAACACA TTTCCGGTGC GGGCTGGAGT GGCGATGCCG AGGCGACCTC	1860
65	GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCCCAAC ATCGTGAACA TGCTGCACGG	1920
	GGTGCCTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA	1980

	GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAA ACTTTTACAA GCGAAGGGAGA	2040
5	ACAGGTTCGA TGACCATCAA CTATCAATTG GGGGATGTGG ACGCTCACGG CGCCATGATC CGCGCTCAGG CCGGGTTGCT GGAGGCCAG CATCAGGCCA TCATTCTGTA TGTGTTGACC	2100 2160
10	GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTCAT TACCCAGTTG GGCGTAACT TCCAGGTGAT CTACGAGCAG GCCAACGCC ACGGGCAGAA GGTGCAGGCT	2220 2280
15	GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGC CTGACACCAG GCCAAGGCCA GGGACGTGGT GTACCGAGTGA AGTTCTCGC GTGATCCTTC GGGTGGCAGT	2340 2400
20	CTAAGTGGTC AGTGCTGGGG TGTTGGTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCAGG TAGGCCGTC CTTCGATCCA	2460 2520
25	TTCGTCGTGT TGTTGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG GAAGATGCCA ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT	2580 2640
30	GTTGGACCAAG ATTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT GGGGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC	2700 2760
35	CCGATCATAT TGGGCAACAA CTGATTGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG	2820 2880
	GGTTCTGCAG CGCTGCCAGG CCGCTGCCGG CAGGGTGGCG CCGATCGCGG CCACCCAGGCC	2940
	GGCGTGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG	3000
	GAAGAACGCC AGCCAGCCGG CCCCCGCTCTC GGCAGGAGGTG ACCTGGATGC CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:14: TbH9FL

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125

5 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160

10 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 15 180 185 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205

20 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240

25 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 30 260 265 270

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285

35 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320

40 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 45 340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
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50 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380

Pro His Ser Pro Ala Ala Gly
 55 385 390

<210> SEQ ID NO:15
 <211> 2287
 <212> DNA
 60 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tri-fusion
 protein Mtb72F(Ra12-TbH9-Ra35 or Mtb32-Mtb39
 fusion)

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 Met His His His His
 1 5

	cat cac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag His His Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln 10	15	20	104
5	gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile 25	30	35	152
10	cga tcg ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc Arg Ser Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe 40	45	50	200
15	ctc ggc ttg ggt gtc gac aac aac ggc aac ggc gca cga gtc caa Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln 55	60	65	248
20	cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly 70	75	80	296
25	gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala 90	95	100	344
30	atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val 105	110	115	392
35	acc tgg caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu 120	125	130	440
40	gcc gag gga ccc ccg gcc gaa ttc atg gtg gat ttc ggg gcg tta cca Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro 135	140	145	488
45	ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser 150	155	160	536
50	ctg gtg gcc gcg gct cag atg tgg gac acg gtg gcg agt gac ctg ttt Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe 170	175	180	584
55	tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly 185	190	195	632
60	tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ser Pro 200	205	210	680
65	tat gtg gcg tgg atg acg gtc acc gcg ggg cag gcc gag ctg acc gcc Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala 215	220	225	728
70	gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu 230	235	240	776
75	acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile 250	255	260	824
80	ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val 265	270	275	872

	aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met 280	285	290	920
5	ttt ggc tac gcc gcg acg gcg acg gcg acg gcg acg ttg ctg ccg Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro 295	300	305	968
10	ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc ctc gag cag Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln 310	315	320	325
15	gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu 330	335	340	1064
20	atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln 345	350	355	1112
25	ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser 360	365	370	1160
30	ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc aac aac cac Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His 375	380	385	1208
35	atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser 390	395	400	405
40	atg ttg aag ggc ttt gct ccg gcg ggc cgc cag gcc gtg caa acc Met Leu Lys Gly Phe Ala Pro Ala Ala Arg Gln Ala Val Gln Thr 410	415	420	1256
45	gag gcg caa aac ggg gtc ccg gcg atg agc tcg ctg ggc agc tcg ctg Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu 425	430	435	1304
50	ggg tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg ggt cgg gcg Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala 440	445	450	1352
55	gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Asn 455	460	465	1400
60	cag gca gtc acc ccg gcg ccg cgg cgg ctg ccg acc agc ctg acc Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr 470	475	480	485
65	agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val 490	495	500	1448
70	ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg 505	510	515	1544
75	gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp 520	525	530	1592
80	atc gcc ccg ccg gcc ttg tcg cag gac ccg ttc gcc gac ttc ccc gcg Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala 535	540	545	1640
85				1688

	ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	1736
	550 555 560 565	
5	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	1784
	570 575 580	
10	acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	1832
	585 590 595	
15	gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	1880
	600 605 610	
20	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	1928
	615 620 625	
25	gcf gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcf atc Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	1976
	630 635 640 645	
30	ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	2024
	650 655 660	
35	ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	2072
	665 670 675	
40	ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	2120
	680 685 690	
45	aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	2168
	695 700 705	
50	tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	2216
	710 715 720 725	
55	<210> SEQ ID NO:16 <211> 729 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:tri-fusion protein Mtb72F (Ra12-TbH9-Ra35 or Mtb32-Mtb39 fusion)	2268
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60	1 5 10 15	
	Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
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65	Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile	
	35 40 45	
	Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	

	50	55	60
	Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu		
	65 70 75 80		
5	Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile		
	85 90 95		
	Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly		
10	100 105 110		
	Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr		
	115 120 125		
15	Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp		
	130 135 140		
	Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly		
	145 150 155 160		
20	Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val		
	165 170 175		
	Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp		
25	180 185 190		
	Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val		
	195 200 205		
30	Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln		
	210 215 220		
	Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu		
	225 230 235 240		
35	Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg		
	245 250 255		
	Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr		
40	260 265 270		
	Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln		
	275 280 285		
45	Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr		
	290 295 300		
	Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly		
	305 310 315 320		
50	Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala		
	325 330 335		
	Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu		
55	340 345 350		
	Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu		
	355 360 365		
60	Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser		
	370 375 380		
	Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr		
	385 390 395 400		
65	Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Arg		
	405 410 415		
	Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser		

420 425 430

Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
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5

Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460

Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
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Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495

15

Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
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Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 20 515 520 525

Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540

Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 25 545 550 555 560

Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575

30

Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590

Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605

35

Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620

Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 40 625 630 635 640

Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655

Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 45 660 665 670

Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685

50

Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
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Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
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Val Val Gly Met Asn Thr Ala Ala Ser
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60

<210> SEQ ID NO:17
 <211> 2190
 <212> DNA
 <213> Mtb72FMutSA

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 ggggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tgttgtcgac 180

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gcaacggcg	cggcgacgtt	gtccgcgtt	gaggaggcgc	cggagatgac	cagcgcgggt	960
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cctcttcca	agctgggtgg	ccctgtggaaag	acggcttcgc	cgcatcggtc	ggccatcgac	1140
aacatgggt	cgatggccaa	caaccacat	tgcgtgacca	actccgggtgt	gtcgatgacc	1200
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cgaccctatg	tgatgccc	tttccggca	gcccggcata	tcgccccg	ggcccttgc	1620
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ttcgatggcg	cgatccacgc	cggtgtatgc	ggccggcccg	tcgtcaacgg	cctaggacag	2160
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<210> SEQ ID NO:18

<211> 729

<212> PRT

40 <213> Mtb72FMutSA

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Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
35 40 45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80

Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95

60 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125

65 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140

Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 5 Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 10 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
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 15 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Val Ile Ala Glu Asn Arg
 20 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 25 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300
 30 Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335
 Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 40 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 45 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
 50 405 410 415
 Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 55 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 60 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 65 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
 500 505 510

Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 5 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 10 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 15 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 20 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 25 Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 30 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 35 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 40 Val Val Gly Met Asn Thr Ala Ala Ser
 725
 45 <210> SEQ ID NO:19
 <211> 1797
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:bi-fusion
 50 protein TbH9-Ra35 (designated Mtb59f)
 <222> (1)..(1791)
 cat atg cat cac cat cac cat atg gtg gat ttc ggg gcg tta cca 48
 His Met His His His His His Met Val Asp Phe Gly Ala Leu Pro
 55 1 5 10 15
 ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg 96
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30
 60 ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt 144
 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 65 tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg 192
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60

	tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro	65	70	75	80	240
5	tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala	85	90	95		288
10	gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	100	105	110		336
15	acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	115	120	125		384
20	ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	130	135	140		432
25	aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc gcg atg Asn Glu Ala Glu Tyr Glu Met Trp Ala Gln Asp Ala Ala Ala Met	145	150	155	160	480
30	ttt ggc tac gcc gcg acg gcg acg gcg acg gcg acg ttg ctg ccg Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro	165	170	175		528
35	ttc gag gag gcg ccg gag atg acc acg gcg ggt ggg ctc ctc gag cag Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln	180	185	190		576
40	gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg aac cag ttg Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Asn Gln Leu	195	200	205		624
45	atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag ccc acg cag Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln	210	215	220		672
50	ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag acg gtc tcg Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser	225	230	235	240	720
55	ccg cat cgg tcg ccg atc acg aac atg gtg tcg atg gcc aac aac cac Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His	245	250	255		768
60	atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc ttg agc tcg Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser	260	265	270		816
65	atg ttg aag ggc ttt gct ccg gcg gcc gca cag gcc gtg caa acc Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr	275	280	285		864
	gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc agc tcg ctg Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu	290	295	300		912
	ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gca aac ttg ggt cgg gcg Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala	305	310	315	320	960
	gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc gcg gcc aac Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Asn	325	330	335		1008

	cag gca gtc acc ccg gcg gcg cgg ctg ccg ctg acc agc ctg acc	1056
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
	340 345 350	
5	agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg	1104
	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
	355 360 365	
10	ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt	1152
	Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg	
	370 375 380	
15	gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat	1200
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
	385 390 395 400	
	atc gcc ccg ccg gcc ttg tcg cag gac ccg ttc gcc gac ttc ccc gcg	1248
	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
	405 410 415	
20	ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg	1296
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	420 425 430	
25	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1344
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	435 440 445	
30	acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac	1392
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	450 455 460	
35	gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1440
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	465 470 475 480	
40	caa acc tac ggc gtc gat gtg gtc ggg tat gac ccg acc cag gat gtc	1488
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	485 490 495	
45	gct gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc	1536
	Ala Val Leu Gln Leu Arg Gly Ala Gly Leu Pro Ser Ala Ala Ile	
	500 505 510	
50	ggt ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	1584
	Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
	515 520 525	
55	ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	1632
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	530 535 540	
	ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag	1680
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
	545 550 555 560	
60	aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	1728
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	565 570 575	
65	tcg ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	1776
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
	580 585 590	
	acg gcc gcg tcc taggatatac	1797
	Thr Ala Ala Ser	
	595	

<210> SEQ ID NO:20
 <211> 596
 <212> PRT
 5 <213> Artificial Sequence
 <223> Description of Artificial Sequence:bi-fusion
 protein TbH9-Ra35 (designated Mtb59f)

10	His	Met	His	His	His	His	His	Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	
	1							10					15			
15	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser
			20					25					30			
20	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe
			35					40					45			
25	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp	Gly	Leu	Thr	Val	Gly
			50				55					60				
30	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala	Ser	Pro
			65				70			75					80	
35	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala
			85				90						95			
40	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	
			100				105						110			
45	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile
			115				120						125			
50	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val
			130				135						140			
55	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met
			145				150				155				160	
60	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro		
			165				170						175			
65	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln
			180				185						190			
70	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu
			195				200						205			
75	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln
			210				215						220			
80	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser
			225				230				235			240		
85	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His
			245				250						255			
90	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser
			260				265						270			
95	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	Gln	Ala	Val	Gln	Thr	
			275				280						285			
100	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser	Leu	Gly	Ser	Ser	Leu
			290				295						300			
105	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Val	Ala	Ala	Asn	Leu	Gly	Arg	Ala	
			305				310				315			320		
110	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	Ala	Trp	Ala	Ala	Ala	Asn

	325	330	335	
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr			
	340	345	350	
5	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val			
	355	360	365	
	Gly Gln Met Gly Ala Arg Ala Gly Gly Leu Ser Gly Val Leu Arg			
10	370	375	380	
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp			
	385	390	395	400
15	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala			
	405	410	415	
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val			
	420	425	430	
20	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly			
	435	440	445	
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His			
25	450	455	460	
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly			
	465	470	475	480
30	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val			
	485	490	495	
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile			
	500	505	510	
35	Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser			
	515	520	525	
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala			
40	530	535	540	
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu			
	545	550	555	560
45	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp			
	565	570	575	
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn			
	580	585	590	
50	Thr Ala Ala Ser			
	595			

55 (2) INFORMATION FOR SEQ ID NO:21: DPV (MTB8.4)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

65	CGTGGCAATG TCGTTGACCG TCGGGGCCGG GGTCGCCTCC GCAGATCCCG TGGACGCGGT	60
	CATTAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG	120
	GGCTGCCGCA CAGTTCAACG CCTCACCGGT GGCGCAGTCC TATTTGCGCA ATTTCCCTCGC	180
	CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC	240

ACAGTACATC	GGCCTGTCG	AGTCGGTTGC	CGGCTCCTGC	AACAACTATT	AAGCCCATGC	300
GGGCCCATC	CCCGCACCG	GCATCGTCG	CGGGGCTAGG	CCAGATTGCC	CCGCTCCTCA	360
ACGGGCCGA	TCCCCGACC	CGGCATCGTC	GCCGGGCTA	GGCCAGATTG	CCCCGCTCCT	420
CAACGGCCG	CATCTCGTGC	CGAATTCCGT	CAGCCCGGGG	GATCCACTAG	TTCTAGAGCG	480
5	GCCGCCACCG	CGGTGGAGCT				500

(2) INFORMATION FOR SEQ ID NO:22: DPV (MTB8.4)

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro		
1										10					15		
20	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	
										25					30		
	Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	
										35					40	45	
25	Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	
										50					55	60	
	Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	
										65					70	75	80
	Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	
										85					90		95

30 (2) INFORMATION FOR SEQ ID NO:23: MSL (MTB9.8)

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGATTCCGA	TAGCGGTTTC	GGCCCTCGA	CGGGCGACCA	CGGCGCGCAG	GCCTCCGAAC	60
GGGGGGCCGG	GACGCTGGGA	TTCGCCGGGA	CCGCAACCAA	AGAACGCCGG	GTCCGGGCCGG	120
50	TCGGGCTGAC	CGCACTGGCC	GGTGATGAGT	TCCGCAACGG	CCCCCGGATG	180
	CGGGGACCTG	GGAGCAGGGC	AGCAACGAGC	CCGAGGGGCC	CGACGGATCG	240
	GAGGCGACGG	CTTACCGCAC	GACAGCAAGT	AACCGAATTG	GGACCCGTAC	300
	GGGTCGAAAG	GAGAGATGTT	ATGAGCCTTT	TGGATGCTCA	TATCCCACAG	360
	CCCAGTCGGC	GTTGGCGCC	AAGGGCGGGC	TGATCGGGCA	CACGATCGGT	420
55	AGGC GGCGAT	GTCGGCTCAG	GGCTTTCACC	AGGGGGAGTC	GTCGGCGGG	480
	CCCATGCCCG	GTTTGCGCG	GGGGCCGCCA	AAGTCAACAC	TTTCAAGGCCG	540
	CGAATCTGGG	TGAGGCCGCC	GGTACCTATG	TGGCCGCCGA	TGCTG	585

60 (2) INFORMATION FOR SEQ ID NO:24: MSL (MTB9.8)

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	Met	Ser	Leu	Leu	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser
	1									10					15	
5	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala
									20	25				30		
	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser
									35	40			45			
10	Ala	Ala	Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Lys	
									50	55			60			
	Val	Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala
									65	70			75		80	
	Gly	Thr	Tyr	Val	Ala	Ala	Asp	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	
									85			90		95		
15	Phe															

(2) INFORMATION FOR SEQ ID NO:25: MTI (MTB9.9A)

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1742 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGCTCTCTT	TCAACGTCA	AAGTTCGGTG	GGCCAGTCGG	CCGCAGCGTGC	ATATGGCAC	60
AATAACGCGT	GTCCCCATGGA	TACCCGGACC	GCACGACGGT	AGAGCGGATC	AGCGCAGGCC	120
35	GTGCCGAAAC	CTACCGCGTC	CACGCTCAGC	CCTGCCCGGT	TGCGGAAGAT	180
	TTCTCATGGT	CGTTAACACT	TCGACGGTGC	GCGCCCCGGC	CGAGCCCAGG	240
	GCAACGCTCG	GCTCCGGCAC	CCGGCGCGCG	GCTGCCAAC	CCCCACGATT	300
	CCGATCACCC	GTGCCATGAC	ATCAGCCGAC	GCTCGATAGT	ACGGCGGCC	360
40	AGATCATCCT	TGAGCTCGGC	CAGCCGGCGG	TCGGTGCCGA	ACAGCGCCAG	420
	CGTGAGGCCA	GCATCGCCTG	CACCACCGC	ACACCCCTGG	CGATCACCAA	480
	GTCGGCAGAT	CGGGACNACN	GTCGATGCTG	TTCAGGTAC	GGAAATCGTC	540
	TCGTCGGGAT	CGCAGACGTC	CTGAACATCG	AGGCCGTCGG	GGTGTGGGC	600
	TCGGTCACGG	GCTTCGTCG	ACCAGAGCCA	GCATCAGATC	GGCGCCGCTG	660
	CACGCTCGT	CGGGITTCAGC	GTCGCGAGCC	GCTCAGCCAG	CCACTCTTGC	720
45	TGCTGGGATT	AATTGGGAGA	GGAAAGACAGC	ATGTCGTTG	TGACCACACA	780
	CTGGCAGCTG	CGGCAGCGAA	CCTACAGGGT	ATTGGCACGA	CAATGAACGC	840
	GCCCGGGCTG	CTCCAACCAC	CGGAGTAGTG	CCCGCAGCCG	CCAGAGCCGT	900
	ACCGCGGCC	AGTTTGTGTC	GCACGCGCAG	ATGTACCAA	CGGTCACTGC	960
50	GCCATTACAG	AAATGTTCGT	GAACACGCTG	GTGGCCAGTT	CTGGCTCATA	1020
	GAGGCGGCCA	ACGCAGCCGC	TGCCGGCTGA	ACGGGCTCGC	ACGAACCTGC	1080
	GGGGAAACATC	CGGAGTTCTC	GGGTCAAGGGG	TTGCGCCAGC	GCCCAGCCGA	1140
	GGCGTCCATA	ACAGCAGACG	ATCTAGGCAT	TCAGTACTAA	GGAGACAGGC	1200
	CACGTTTAT	GACGGATCCG	CATGCATGC	GGGACATGGC	GGGCGTTTT	1260
55	CCCAAGACGGT	GGAGGACGAG	GCTCGCCGGA	TGTGGGCGTC	CGCGAAAAC	1320
	CGGGCTGGAG	TGGCATGGCC	GAGGCGACCT	CGCTAGACAC	ATTTCGGGTG	1380
	CGTTTCGCAA	CATCGTGAAC	ATGCTGCACC	GGGTGCGTGA	CGGGCTGGTT	1440
	ACAANTACGA	ACAGCAAGAG	CAGGCCCTCC	AGCAGATCCT	GAGCAGNTAG	1500
	CACAGCTGNG	TACGNNTCT	CACATTAGGA	GAACACCAAAT	ATGACGATTA	1560
60	CGGGGACGTC	GACGCTCATG	GCGCCATGAT	CCGCGCTCAG	GCGCGTCGC	1620
	GCATCAGGCC	ATCGTTCGTG	ATGTGTTGGC	CGCGGGTGAC	TTTTGGGGCG	1680
	GGTGGCTTGC	CAGGAGTTCA	TTACCCAGTT	GGGCCGTAAC	TTCCAGGTGA	1740
	GG					1742

65 (2) INFORMATION FOR SEQ ID NO:26: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2836 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium tuberculosis*

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTGATTCCG	TTCGGCGCGC	CGCCGAAGAC	CACCAACTCC	GCTGGGTGG	TCGCACAGGC	60
GGTTGCGTCG	GTCAGCTGGC	CGAACATCCAA	TGATTGGTGG	CTCNGTGC GG	TTGCTGGGCT	120
CGATTACCCC	CACGGAAAGG	ACGACGATCG	TTCGTTTGCT	CGGTCA GTCG	TACTTGGCGA	180
15 CGGGCATGGC	GCGGTTTCTT	ACCTCGATCG	CACAGCAGCT	GACCTTCGGC	CCAGGGGGCA	240
CAACGGCTGG	CTCCGGCGGA	GCTGGTACCG	CAACGCCACA	ATT CGCCGGC	CTGGGTGCAG	300
GCCCGGCGGT	GTCGGCGAGT	TTGGCGCGGG	CGGAGCGCGT	CGGGAGGTTG	TCGGTGC CGC	360
CAAGTTGGC	CGTCGGCGCT	CCGGCCTTCG	CGGAGAA GGC	TGAGGGCGGG	ACGCCGATGT	420
20 CCGTCATCGG	CGAACGGTCC	AGCTCGGGTC	AGGGAGGGCT	GCTTCGAGGC	ATACCGCTGG	480
CGAGAGCGGG	GCGGCC TACA	GGCCCTTCG	CTCAGCGATA	CGGGTCCGC	CACAGCGTGA	540
TTACCCGGTC	TCCGTCGGCG	GGATAGCTT	CGATCCGGTC	TGCGCGGCCG	CCGGAAATGC	600
TGCAGATAGC	GATCGACCGC	GCCGGT CGGT	AAACGCCGCA	CACGGCACTA	TCAATGCCA	660
CGGGGGCGGT	TGATGCCAAA	TTGACCGTCC	CGACGGGGCT	TTATCTGC GG	CAAGATTTCA	720
25 TCCCCAGCCC	GGTCGGTGGG	CCGATAAAATA	CGCTGGTCAG	CGCGACTCTT	CCGGCTGAAT	780
TCGATGCTCT	GGGCGCCCGC	TCGACGCCGA	GTATCTCGAG	TGGGCCGCAA	ACCCGGTCAA	840
ACGCTGTTAC	TGTGGCGTTA	CCACAGGTGA	ATT TGCGGTG	CCAAC TGGTG	AACACTTGCG	900
AACGGGTGGC	ATCGAAATCA	ACTTGTGCG	TTGCAGTGAT	CTACTCTCTT	GCAGAGAGCC	960
GTTGCTGGGA	TTAATTGGGA	GAGGAAGACA	GCATGTGCTT	CGTGACCACA	CAGCCGGAAG	1020
30 CCCTGGCAGC	TGCGGGCGCG	AA CCTACAGG	GTATTGGCAC	GACAATGAAC	CCCCAGAACG	1080
CGGCGCGGC	TGCTCCA ACC	ACCGGAGTAG	TGCGCGCAGC	CGCCGATGAA	GTATCAGCGC	1140
TGACCGCGGC	TCAGTTGCT	GGCACCGCGC	AGATGTACCA	AACGGTCAGC	GCCCAGGCC	1200
CGGCCATTCA	CGAAATGTT	GTGAACACGC	TGGTGGCCAG	TTCTGGCTCA	TACGCGGCCA	1260
CCGAGGCGGC	CAACCGAGCC	GCTGCCGGCT	GAACGGGCTC	GCACGAACCT	GCTGAAGGAG	1320
AGGGGAAACA	TCCGGAGTT	TCGGGTCA GG	GGTTGCGCCA	GCGCC CAGCC	GATT CAGCTA	1380
35 TCGGCGTCA	TAACAGCAGA	CGATCTAGGC	ATT CAGTACT	AAGGAGACAG	GCAACATGGC	1440
CTCACGTTT	ATGACGGATC	CGCATGCGAT	GCGGGACATG	GCGGGCCGTT	TTGAGGTGCA	1500
CGCCCAGACG	GTGGAGGACG	AGGCTCGCCG	GATGTGGCG	TCCCGC AAAA	ACATTTCCGG	1560
TGCGGGCTGG	AGTGGCATGG	CGGAGGC GAC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
GGCGTTTCGC	AACATCGTGA	ACATCGTGC	CGGGGTGCGT	GACGGGCTGG	TTCGCGACGC	1680
40 CAACAACTAC	GAACAGCAAG	AGCAGG CCTC	CCAGCAGATC	CTGAGCAGCT	AGC GCGAAA	1740
GCCACAGCTG	CGTACGCTTT	CTCACATTAG	GAGAACACCA	ATATGACGAT	TAATTACCA	1800
TTCGGGGACG	TGCGAGCTCA	TGGCGCATG	ATCCGGCTC	AGGGGGCGTC	GCTTGAGGCG	1860
GAGCATCAGG	CCATCGTTG	TGATGTGTT	GCGCGGGTG	ACTTTGGGG	CGGCGCCGGT	1920
TCGGTGGCTT	GCCAGGAGT	CATTACCCAG	TTGGGCCGTA	ACTTCCAGGT	GATCTACGAG	1980
45 CAGGCCAACG	CCCACGGGCA	GAAGGTGCA G	GCTGCCGGCA	ACAACATGGC	GCAAACCGAC	2040
AGCGCCGTCG	GCTCCAGCTG	GGCCCTAAAAC	TGAAC TTCA G	TCGCGGCAGC	ACACCAACCA	2100
GCCGGTGTG	TGCTGTGTCC	TGCAGTTAAC	TAGCACTCGA	CCGCTGAGGT	AGCGATGGAT	2160
CAACAGAGTA	CCCGCACCGA	CATCACCGTC	AACGTGACG	GCTTCTGGAT	GCTTCAGGCG	2220
50 CTACTGGATA	TCCGCCACGT	TGCGCTGAG	TTACGTTGCC	GGCGTACGT	CTCCACCGAT	2280
TCCAATGACT	GGCTAAACGA	GCACCCGGGG	ATGGCCGTCA	TGCCCGAGCA	GGGCATTGTC	2340
GTCAACGACG	CGGTCAACGA	ACAGGTGCGT	GCCCCGGATGA	AGGTGCTTG	CGCACCTGAT	2400
CTTGAAGTCG	TGCGCTGTCT	GTCACGCGGG	AA GTTGCTGT	ACGGGGTCA	AGACGACGAG	2460
AACCAGCGC	CGGGTTCGCG	TGACATCCCT	GACAATGAGT	TCCGGGTGGT	GTTGGCCCGG	2520
55 CGAGGCCAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
ACGGTCTCGG	ATAGCGCCTC	GATCGCCGA	CTGGTAATGG	ACGGTCTGG	GTG GATT CAC	2640
CACGCCGACC	CAGCCCGAT	CAACGCCGTC	AA CGTGCCAA	TGGAGGAGAT	CTCGTGC CGA	2700
ATT CGGCACG	AGGCACGAGG	CGGTGTCGGT	GACGACGGGA	TCGATCACGA	TCATCGACCG	2760
GCCGGGATCC	TTGGCGATCT	CGTTGAGCAC	GACCCGGGCC	CGCGGGAAAGC	TCTGCGACAT	2820
60 CCATGGGTT	TTCCCC					2836

(2) INFORMATION FOR SEQ ID NO:27: MTI (MTB9.9A)

- 65 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10 Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
15 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
20 85 90

(2) INFORMATION FOR SEQ ID NO:28: HTCC#1

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

35 CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGACG 60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT 120
TCGAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTCGG 180
CCGGCGACAA ATACGCCGGC AAAAACCGCA ACCACGTGAA TTTTTTCCAG GAACTGGCAG 240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACCGCGTC CAGACGACCC 300
40 GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTCGT GCGCCCGGTG GCTGTGGACC 360
TGACCTACAT CCCGTCGTC GGGCACGCC TATCGGCCG CTTCCAGGC CGCTTTTCGCG 420
CGGGCGCGAT GGCCCTAGTG GGGGGCGCC TTGCTCTACTT GGTCTGAAA ACGCTGATCA 480
ACCGCAGCTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCGCG GCGGCCATTG 540
45 CGGACATCAT TTCGGATGTG GCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGAGT 600
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTGGGA CAAGCTCACG GGGTGGGTGA 660
CCGGACTGTT CTCTCGAGGG TGGTCGAACC TGGAGTCCTT CTTGCGGGC GTCCCCGGCT 720
TGACCGGGCGC GACCAGCGGC TTGTCGCAAG TGACTGGCTT GTTCGGTGCG GCGGGTCTGT 780
CCGCATCGTC GGGCTTGCT CACCGGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCCGCC 840
50 TGGCCGGCAT TGGGGGCGGG TCCGGTTTG GGGGCTTGCC GAGCCTGGCT CAGGTCCATG 900
CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGGC GCGCTGCCG 960
AGCAGGGTGG CGGGCAGTCG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGGCGAC 1020
CCGTAGGCAT GGGGGCATG CACCCCTCTT CGGGGGCGTC GAAAGGGACG ACGACGAAGA 1080
AGTACTCGGA AGGCGCGGCG GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG 1140
ACGCGGGCGG TGGGCAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA 1200

55

(2) INFORMATION FOR SEQ ID NO:29: HTCC#1

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
 1 5 10 15
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
 20 25 30
 5 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
 35 40 45
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
 50 55 60
 10 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65 70 75 80
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
 85 90 95
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
 100 105 110
 15 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 120 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 20 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 25 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 30 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 35 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 40 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 45 Lys Gly Thr Thr Thr Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 50 Lys Val Leu Val Arg Asn Val Val
 385 390

(2) INFORMATION FOR SEQ ID NO:30: MTCC#2

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

65	GAGGTTGCTG GCAATGGATT TCGGGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA	60
	TTCCGGTCCG GGGCCGGAGT CGATGCTAGC CGCCGCGGCC GCCTGGGACG GTGTGGCCGC	120
	GGAGTTGACT TCCGCCGCGG TCTCGTATGG ATCGGGTGGTG TCGACGCTGA TCGTTGAGCC	180
	GTGGATGGGG CCGCGGGCGG CCGCGATGGC GGCGCGGGCA ACGCCGTATG TGGGGTGGCT	240

	GGCCGCCACG	GCGGCCTGG	CGAAGGAGAC	GGCCACACAG	GCGAGGGCAG	CGGCAGGAAGC	300
	GTTTGGGACG	GCGTCGCGA	TGACGGTGC	ACCATCCCTC	GTGCGGCCA	ACCGCAGCCG	360
	GTTGATGTCG	CTGGTCGCG	CGAACATTCT	GGGGAAAC	AGTCGCGCA	TCGCGGCTAC	420
5	CCAGGCCAG	TATGCCAAA	TGTGGGCCA	AGACGCTG	GTGATGTACA	GCTATGAGGG	480
	GGCATCTGCG	GCCCGTCTGG	CGTTGCCGCG	GTTCACTCCA	CCCCTGCAAG	GCACCGGCC	540
	GGCCGGCCCC	GCGGCCGAG	CCGCGGCCAG	CCAAGCCGCC	GGTGCGGCG	CCGTTGCCGA	600
	TGCACAGGGC	ACACTGGCCC	AGCTGCC	GGGGATCCTG	AGGCACATT	TGTCGCAATT	660
	GGCCGCCAAC	GCTGATCCGC	TGACATCGGG	ACTGTTGGGG	ATCGCGTCGA	CCCTCAACCC	720
10	GCAAGTCGGA	TCCGCTCAGC	CGATAGTGTAT	CCCCACCCCG	ATAGGGGAAT	TGGACGTGAT	780
	CGCGCTCTAC	ATTGCATCCA	TCGCGACCGG	CAGCATTGCG	CTCGCGATCA	CGAACACGGC	840
	CAGACCCCTGG	CACATCGGCC	TATACTGGAA	CGCCGGCGGG	CTGGGACCGA	CGCAGGGCCA	900
	TCCACTGAGT	TCGGCGACCG	ACGAGCCGGA	GCCGCACTGG	GGCCCTTCG	GGGGCGCGGC	960
	GCCGGTGTCC	GCGGGCGTCG	GCCACGCAGC	ATTAGTCGGA	GCGTTGTCGG	TGCCGCACAG	1020
15	CTGGACCACG	GCCGCCCGG	AGATCCAGCT	CGCCGTTCA	GCAACACCCA	CCTTCAGCTC	1080
	CAGCGCCGGC	GCCGACCCGA	CGGCCCTAA	CGGGATGCCG	GCAGGCCCTGC	TCAGCGGGAT	1140
	GGCTTTGGCG	AGCCTGGCCG	CACGCGGCAC	GACGGGCGGT	GGCGGCACCC	GTAGCGGCAC	1200
	CAGCACTGAC	GGCCAAGAGG	ACGGCCGCAA	ACCCCCGTA	GTTGTGATTA	GAGAGCAGCC	1260
	GCCGCCCGGA	AACCCCCCGC	GGTAAAAGTC	CGGCAACCGT	TCGTCGCCGC	GCGGAAAAATG	1320
20	CCTGGTGAGC	GTGGTATCC	GACGGGCCGT	TCACACCGCT	TGTAGTAGCG	TACGGCTATG	1380
	GACGACGGTG	TCTGATTCT	CGCGGCTAT	CAGAGCGATT	TTGCTCGCAA	CCTCAGCAA	1440
	G						1441

(2) INFORMATION FOR SEQ ID NO:31: MTCC#2

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 423 amino acids
	(B) TYPE: amino acid
30	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
	Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
	1 5 10 15
	Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp
	20 25 30
40	Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
	35 40 45
	Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala
	50 55 60
	Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
	65 70 75 80
45	Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala
	85 90 95
	Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
	100 105 110
50	Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
	115 120 125
	Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
	130 135 140
55	Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
	145 150 155 160
	Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
	165 170 175
	Ala Gly Pro Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
	180 185 190
60	Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
	195 200 205
	Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
	210 215 220
65	Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
	225 230 235 240
	Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
	245 250 255
	Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile

	260	265	270
	Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly		
	275	280	285
5	Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu		
	290	295	300
	Pro Glu Pro His Trp Gly Pro Phe Gly Ala Ala Pro Val Ser Ala		
	305	310	315
	Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser		
	325	330	335
10	Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro		
	340	345	350
	Thr Phe Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met		
	355	360	365
15	Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg		
	370	375	380
	Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly		
	385	390	395
	Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro		
	405	410	415
20	Pro Pro Gly Asn Pro Pro Arg		
	420		

(2) INFORMATION FOR SEQ ID NO:32: ESAT-6

25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 154 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
35	ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA	60
	AATGTCACGT CCATTCCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA	120
	GC GG CCGCTGGG GCGGTAGCGG TTCGGAAGCG TACC	154

(2) INFORMATION FOR SEQ ID NO:33: ESAT-6

40	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 51 amino acids			
	(B) TYPE: amino acid			
	(C) STRANDEDNESS: single			
45	(D) TOPOLOGY: linear			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:			
50	Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ser			
	1	5	10	15
	Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly			
	20	25	30	
	Lys Gln Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser			
	35	40	45	
55	Glu Ala Tyr			
	50			

(2) INFORMATION FOR SEQ ID NO:34: Tb38-1

60	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 327 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
65	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	

	CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTC GAGCGGATCT	60
	CCGGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTCG TTGCAGGGCC	120
	AGTGGCGCGG CGCGGCGGGG ACGGCCGCCC AGGCCGCGGT GGTGCCTTC CAAGAACAG	180
5	CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGGCGTCC	240
	AATACTCGAG GGCGACGAG GAGCAGCAGC AGGCCTGTC CTCGCAAATG GGCTTCTGAC	300
	CCGCTAATAC GAAAAGAAC GGAGCAA	327

(2) INFORMATION FOR SEQ ID NO:35: Tb38-1

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20	Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile	
	1 5 10 15	
	Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly	
	20 25 30	
	Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala	
	35 40 45	
25	Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu	
	50 55 60	
	Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg	
	65 70 75 80	
30	Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe	
	85 90 95	

(2) INFORMATION FOR SEQ ID NO:36: TbRa3

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

45	GAATTGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC	60
	GGCGCGGGAG CGGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCCGCG TCGCTCGGGT	120
	CATTGAGCAG GACATGGCCG TGAGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA	180
	AGTGTGTTTC AAGATGAGGC CGGGCGAACCG GCGCTAGCAC GGGCCGGCGA GCAAGACGCA	240
	AAATCGCACG GTTGCGGTT GATTGCGCG ATTTTGTCG TGCTCGCCGA GGCCTACCAG	300
	GCGCGGCCCA GGTCCCGGTG CTGCGTATC CAGGCGTGCA TCGCGATTCC GGCAGGCCACG	360
50	CCGGAGTTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGGNGAGC TGATCGATGA	420
	CCGTGGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA	480
	AGCGTCCGTA GGCGCGGTG CTGACCGGCT CTGCCTGGCG CCTCAGTGC GCGAGCGAGC	540
	GG	542

55 (2) INFORMATION FOR SEQ ID NO:37: TbRa3

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

65	Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala	
	1 5 10 15	
	Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val	
	20 25 30	

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 5 Pro Arg
 65

10 (2) INFORMATION FOR SEQ ID NO:38: 38 kD

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTT TCCTCGCCGA	60
20 AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAACG	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTGCATA CGCTGTTGGC	180
25 CGTGTGACCC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACACCAGAG	240
CGGTTCGCCT GAAACGGGCG CCGGCGCCGG TACTGTCGCG ACTACCCCCG CGTCGTCGCC	300
30 GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
GGCCTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCCGCCG CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
35 GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT	600
40 GGCGGCCATG TACCAGGGCA CCATAAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
CCCCGGCGTG AACCTGCCCG GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTCACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
45 GCCCGGCTTC GGCACCCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
CAACGGCGGC ATGGTACCG GTTGCACCGA GACACGGGC TGCGTGGCCT ATATCGGCAT	900
50 CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC	960
TGGCAATTTC TTGTTGCCCG ACGGCGAAAG CATTCAAGCC GCGGCGGCTG GCTTCGCATC	1020
GAAAACCCCG GCGAACCAAG CGATTCGAT GATCGACGGG CCCGCCCCGG ACGGCTACCC	1080
55 GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCGC CCACCGCGCA	1140
GACCTTGCAG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAAGGCCT CGTTCCCTCGA	1200
60 CCAGGTTCAT TTCCAGCCGC TGCCGCCCGC GGTGGTGAAG TTGCTGACG CGTTGATCGC	1260
GACGATTTC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG	1320
GCTGCTTGC GGAGCATGCT GGCGCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC	1380
65 CGGTGGTTGG GTGGGATAGG TCGGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG	1440
GTGCTGGTCA TCGAGGCGAT GGGTGCATC AGGCTCAACG GGTTGCATTT CTTCACCGCC	1500

	ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC	1560
	CGGTCGGCGC CTACTACGGG CGCTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA	1620
5	TCGCCCTGAT CATCGGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC	1680
	TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA	1740
10	GCGTGGTCGT CGGTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG	1800
	CTCCGGTGAT CGCTCACAAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC	1860
	CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTGTT GGCGGTGATG GTCGTTCCCA	1920
15	TTATGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCCG CGGGAGGGCG	1980
	CGATCGGGAA TTC	1993

20 (2) INFORMATION FOR SEQ ID NO:39: 38 kD

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30	Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro	
	1 5 10 15	
	Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser	
	20 25 30	
35	Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser	
	35 40 45	
40	Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu	
	50 55 60	
	Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr	
	65 70 75 80	
45	Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala	
	85 90 95	
	Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly	
	100 105 110	
50	Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser	
	115 120 125	
	Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys	
55	130 135 140	
	Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr	
	145 150 155 160	
60	Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro	
	165 170 175	
	Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr	
	180 185 190	
65	Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly	
	195 200 205	

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220

5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255

10 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285

15 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300

20 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335

25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365

30 Ile Ala Thr Ile Ser Ser
 370

35 (2) INFORMATION FOR SEQ ID NO:40: DPEP

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

45	ATGCATCACCATCA CATGCGATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA	60
	CGATTGGCGG CACTGGCTAT CGCGCGATG GCCAGGCCA GCCTGGTGC CGTTGCGGTG	120
	CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCGCGCTCG	180
	CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGCGACAC CTGTTGCCCC CCCACCACCG	240
	GCCGCCGCCA ACACGCCGAA TGCCCAGCGG GGCATCCCCA ACGCAGCAC TCCGCCGGCC	300
50	GACCGAACG CACCGCCGCC ACCTGTCTT GCCCCAACG CACCCCAACC TGTCGGATC	360
	GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCTGCTG GCTGGGTGGA GTCTGACGCC	420
	GCCCACCTCG ACTACGGTTT ACACACTCTC AGCAAAACCA CGGGGGACCC GCCATTTC	480
	GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAG	540
	CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCCGG CCCGGTTGGG CTCGGACATG	600
55	GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC	660
	GCCAACGGGG TGTCTGGAAG CGCGCTGTAT TACGAAGTCA AGTCAGCGA TCCGAGTAAG	720
	CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGCGAACGC ACCGGACGCC	780
	GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAAACCC GGTGGACAAG	840
	GGCGCGGCCA AGGCCTGGC CGAATCGATC CGGCCCTTGG TCGCCCCGCC GCCGGCGCCG	900
60	GCACCGGCTC CTGCGAGAGCC CGCTCCGGCG CCGGCGCCGG CGGGGAAAGT CGCTCCTACC	960
	CCGACGACAC CGACACCGCA CGGGACCTTA CGGGCCTGA	999

65 (2) INFORMATION FOR SEQ ID NO:41: DPEP

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5 Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30
10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60
15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110
20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115 120 125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140
25 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190
30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220
35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270
40 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300
45 Ala Glu Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

50 (2) INFORMATION FOR SEQ ID NO:42: TbH4

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60 CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTGCCGGG TTTCCCCACC 60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC 120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCACT TTAGCGACGA TAATGGCTAT 180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
AGATTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
65 CCATCACACC GTGCGAACTC ACGGNNGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG 360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT 420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
ACAAACGACGG CGAAGGAAC GTGCAGGCAG AATCGGCCGG GGCGCTCGGA GGGGACAGTT 540

CGGCCGAAC AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCAATGGATC 600
TCAAAGAACG GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG 660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG 702

5

(2) INFORMATION FOR SEQ ID NO:43: TbH4

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15
Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30
20 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45
Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60
25 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80
Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95
Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100 105 110
30 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115 120 125
Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
130 135 140
35 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145 150 155 160
Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165 170 175
Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180 185 190
40 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195 200 205
Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220
45 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270
50 Leu Pro Gly Phe Asp Glu Gly Gly Leu Arg Pro Xaa Lys
275 280 285

55 (2) INFORMATION FOR SEQ ID NO:44: DPPD

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: Genomic DNA

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCGCTTGTG 60
TTTCCTGCCT CGGGTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGA CATGACGAAA 120
GGCTATTGCC CGGGTGGCCG ATGGGGTTT GGCGACTTGG CCGTGTGCGA CGGCGAGAAG 180

TACCCCGACG GCTCGTTTG GCACCAGTGG ATGCAAACGT GGTTTACCGG CCCACAGTT	240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC	300
GGTGGGGCAA TTCCGTCCGA GCAGCCCCAAC GCTCCCTGA	339

5

(2) INFORMATION FOR SEQ ID NO:45: DPPD

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala	
1 5 10 15	
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp	
20 25 30	
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp	
35 40 45	
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly	
50 55 60	
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe	
65 70 75 80	
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro	
85 90 95	
30 Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro	
100 105 110	

<210> SEQ ID NO:46	
<211> 921	
<212> DNA	
<213> Artificial Sequence	
<223> Description of Artificial Sequence:tri-fusion	
protein DPV-MTI-MSL (designated Mtb31f)	
40 <222> (1)..(900)	
cat atg cat cac cat cac cat gat ccc gtg gac gcg gtc att aac	48
His Met His His His His Asp Pro Val Asp Ala Val Ile Asn	
1 5 10 15	
45 acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat	96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp	
20 25 30	
50 ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat	144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr	
35 40 45	
55 ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc	192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Gln Arg Ala Ala Met Ala	
50 55 60	
60 gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc	240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val	
65 70 75 80	
65 gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat	288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn	
85 90 95	
65 tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag	336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln	
100 105 110	

Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 50 55 60

5 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65 70 75 80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 85 90 95

10 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
 115 120 125

15 Ala Ala Gly Asp Phe Trp Gly Gly Ser Val Ala Cys Gln Glu
 130 135 140

20 Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala
 145 150 155 160

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln
 165 170 175

25 Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu
 180 185 190

Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 195 200 205

30 Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala
 210 215 220

35 Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln
 225 230 235 240

Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu
 245 250 255

40 Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val
 260 265 270

Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His
 275 280 285

45 His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys
 290 295

50 <210> SEQ ID NO:48
 <211> 2168
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tetra-fusion
 55 protein DPV-MTI-MSL-MTCC2 (designated Mtb71f)
 <222> (1)..(2133)

cat atg cat cac cat cac cat gat ccc gtg gac gcg gtc att aac 48
 His Met His His His His Asp Pro Val Asp Ala Val Ile Asn
 60 1 5 10 15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30

65 ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

	ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc	192
	Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala	
5	50 55 60	
	gcg caa ttg caa gct gtg ccg ggg ggc gca cag tac atc ggc ctt gtc	240
	Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val	
	65 70 75 80	
10	gag tcg gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat	288
	Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn	
	85 90 95	
15	tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag	336
	Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln	
	100 105 110	
20	gcg gcg tcg ctt gag ggc gag cat cag gcc atc gtt cgt gat gtg ttg	384
	Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu	
	115 120 125	
	gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag	432
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu	
25	130 135 140	
	ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc	480
	Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala	
	145 150 155 160	
30	aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa	528
	Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln	
	165 170 175	
35	acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
	180 185 190	
40	gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc	624
	Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala	
	195 200 205	
	aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala	
	210 215 220	
45	atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag	720
	Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln	
	225 230 235 240	
50	gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu	
	245 250 255	
55	ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg	816
	Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
	260 265 270	
60	gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc atg	864
	Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met	
	275 280 285	
	gat ttc ggg ctt tta cct ccg gaa gtg aat tca agc cga atg tat tcc	912
	Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser	
	290 295 300	
65	ggt ccg ggg ccg gag tcg atg cta gcc gcc gcg gcc tgg gac ggt	960
	Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp Gly	
	305 310 315 320	

	gtg gcc gcg gag ttg act tcc gcc gcg gtc tcg tat gga tcg qtg qtg Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val 325 330 335	1008
5	tcg acg ctg atc gtt gag ccg tgg atg ggg ccg gcg gtc gac atg Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Met 340 345 350	1056
10	gcg gcc gcg gca acg ccg tat gtg ggg tgg ctg gcc gcc acg gcg gcg Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala 355 360 365	1104
15	ctg gcg aag gag acg gca aca cag gcg agg gca gcg gcg gaa gcg ttt Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Glu Ala Phe 370 375 380	1152
20	ggg acg gcg ttc gcg atg acg gtg cca cca tcc ctc gtc gcg gcc aac Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn 385 390 395 400	1200
	cgc agc cgg ttg atg tcg ctg gtc gcg gcg aac att ctg ggg caa aac Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn 405 410 415	1248
25	agt gcg gcg atc gcg gct acc cag gcc gag tat gcc gaa atg tgg gcc Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala 420 425 430	1296
30	caa gac gct gcc gtg atg tac agc tat gag ggg gca tct gct gcg gcc Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala 435 440 445	1344
35	tcg gcg ttg ccg ccg ttc act cca ccc gtg caa ggc acc ggc ccg gcc Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala 450 455 460	1392
40	ggg ccc gcg gcc gca gcc gcg acc caa gcc gcc ggt gcg ggc gcc Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala 465 470 475 480	1440
	gtt gcg gat gca cag gcg aca ctg gcc cag ctg ccc ccg ggg atc ctg Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu 485 490 495	1488
45	agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg aca tcg Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser 500 505 510	1536
50	gga ctg ttg ggg atc gcg tcg acc ctc aac ccg caa gtc gga tcc gct Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala 515 520 525	1584
55	cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala 530 535 540	1632
60	ctc tac att gca tcc atc gcg acc ggc agc att gcg ctc gcg atc acg Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr 545 550 555 560	1680
	aac acg gcc aga ccc tgg cac atc ggc cta tac ggg aac gcc ggc ggg Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly 565 570 575	1728
65	ctg gga ccg acg cag ggc cat cca ctg agt tcg gcg acc gac gag ccg Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro 580 585 590	1776

gag ccg cac tgg ggc ccc ttc ggg ggc gcg gcg ccg gtg tcc gcg ggc 1824
 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
 595 600 605

5 gtc ggc cac gca gca tta gtc gga gcg ttg tcg gtg ccg cac agc tgg 1872
 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
 610 615 620

10 acc acg gcc gcc ccg gag atc cag ctc gcc gtt cag gca aca ccc acc 1920
 Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
 625 630 635 640

15 ttc agc tcc agc gcc ggc gac ccg acg gcc cta aac ggg atg ccg 1968
 Phe Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
 645 650 655

20 gca ggc ctg ctc agc ggg atg gct ttg gcg agc ctg gcc gca cgc ggc 2016
 Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
 660 665 670

25 acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa 2064
 Thr Thr Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
 675 680 685

30 ccc gga aac ccc ccg cgg taagatttct aaatccatca cactggcggc cgctcgag 2168
 Pro Gly Asn Pro Pro Arg
 705 710

35 <210> SEQ ID NO:49
 <211> 710
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tetra-fusion
 40 protein DPV-MTI-MSL-MTCC2 (designated Mtb71f)

His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn
 1 5 10 15

45 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
 20 25 30

Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
 35 40 45

50 Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
 50 55 60

55 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
 65 70 75 80

Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
 85 90 95

60 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 100 105 110

Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu
 115 120 125

65 Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu
 130 135 140

	Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala			
145	150	155	160	
5	Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln			
	165	170	175	
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu			
	180	185	190	
10	Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala			
	195	200	205	
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala			
	210	215	220	
15	Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln			
	225	230	235	240
20	Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu			
	245	250	255	
	Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val			
	260	265	270	
25	Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile Met			
	275	280	285	
	Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr Ser			
	290	295	300	
30	Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Trp Asp Gly			
	305	310	315	320
	Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val			
	325	330	335	
35	Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met			
	340	345	350	
40	Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala			
	355	360	365	
	Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe			
	370	375	380	
45	Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn			
	385	390	395	400
	Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn			
	405	410	415	
50	Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala			
	420	425	430	
55	Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala			
	435	440	445	
	Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala			
	450	455	460	
60	Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala			
	465	470	475	480
	Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu			
	485	490	495	
65	Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser			
	500	505	510	

Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala
515 520 525

5 Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala
530 535 540

Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr
545 550 555 560

10 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly
565 570 575

Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro
580 585 590

15 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala Gly
595 600 605

20 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
610 615 620

Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
625 630 635 640

25 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
645 650 655

Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
660 665 670

30 Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
675 680 685

35 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
690 695 700

Pro Gly Asn Pro Pro Arg
705 710

40